

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/870,122DATE: 12/05/2001
TIME: 10:25:07Input Set : A:\PCT-US99-28826 Sequence listing.txt.txt
Output Set: N:\CRF3\11212001\I870122.raw

ENTERED

4 <110> APPLICANT: Regents of the University of Minnesota et al.
6 <120> TITLE OF INVENTION: Streptococcal C5a peptidase vaccine
8 <130> FILE REFERENCE: 600.450W01
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/870,122
C--> 10 <141> CURRENT FILING DATE: 2001-05-30
10 <150> PRIOR APPLICATION NUMBER: US 09/206,898
11 <151> PRIOR FILING DATE: 1998-12-07
13 <150> PRIOR APPLICATION NUMBER: US 08/589,756
14 <151> PRIOR FILING DATE: 1996-01-22
16 <160> NUMBER OF SEQ ID NOS: 23
18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1164
22 <212> TYPE: PRT
23 <213> ORGANISM: Streptococcus pyogenes
25 <400> SEQUENCE: 1
26 Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
27 1 5 10 15
28 Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
29 20 25 30
30 Thr Val Thr Glu Asp Thr Pro Ala Thr Glu Gln Ala Val Glu Thr Pro
31 35 40 45
32 Gln Pro Thr Thr Val Ser Glu Glu Val Pro Ser Ser Lys Glu Thr Lys
33 50 55 60
34 Thr Pro Gln Thr Pro Asp Asp Ala Glu Glu Thr Val Ala Asp Asp Ala
35 65 70 75 80
36 Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Pro Asp Thr Ser Ala
37 85 90 95
38 Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys
39 100 105 110
40 Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
41 115 120 125
42 Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
43 130 135 140
44 Lys Ala Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys
45 145 150 155 160
46 Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
47 165 170 175
48 Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu
49 180 185 190
50 His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
51 195 200 205
52 Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu
53 210 215 220
54 Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg
55 225 230 235 240
56 Asn Tyr Ala Gln Ala Ile Arg Asp Ala Val Asn Leu Gly Ala Lys Val

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57	245	250	255
58	Ile Asn Met Ser Phe Gly Asn Ala Ala	Leu Ala Tyr Ala Asn	Leu Pro
59	260	265	270
60	Asp Glu Thr Lys Lys Pro Phe Val	Tyr Ala Lys Ser Lys	Gly Val Arg
61	275	280	285
62	Ile Val Thr Thr Ala Gly Asn Asp Ser	Ser Phe Gly Gly	Lys Thr Arg
63	290	295	300
64	Leu Pro Leu Ala Asp His Pro Asp Tyr	Gly Val Val Gly	Thr Pro Ala
65	305	310	315
66	Ala Ala Asp Ser Thr Leu Thr Val Ala	Ser Tyr Ser Pro Asp	Asn Gln
67	325	330	335
68	Leu Thr Glu Thr Ala Met Val Lys	Thr Asp Asp Gln Gln	Asp Lys Glu
69	340	345	350
70	Met Pro Val Leu Ser Thr Asn Arg	Phe Glu Pro Asn Lys	Ala Tyr Asp
71	355	360	365
72	Tyr Ala Tyr Ala Asn Arg Gly	Met Lys Glu Asp Asp	Phe Lys Asp Val
73	370	375	380
74	Lys Gly Lys Ile Ala Leu Ile	Glu Arg Ser Asp Ile	Asp Phe Thr Asp
75	385	390	395
76	Lys Ile Ala Asn Ala Lys Lys	Ala Gly Ala Val	Gly Val Leu Ile Tyr
77	405	410	415
78	Asp Asn Gln Asp Lys Gly Phe Pro	Ile Glu Leu Pro Asn Val	Asp Gln
79	420	425	430
80	Met Pro Ala Ala Phe Ile Ser Arg	Lys Asp Gly Leu	Leu Leu Lys Asp
81	435	440	445
82	Asn Ser Gln Lys Thr Ile Thr	Phe Asn Ala Thr Pro	Lys Val Leu Pro
83	450	455	460
84	Thr Ala Ser Gly Thr Lys Leu Ser Arg	Phe Ser Ser Trp	Gly Leu Thr
85	465	470	475
86	480	485	495
87	Ala Asp Gly Asn Ile Lys Pro Asp Ile	Ala Ala Pro Gly Gln Asp Ile	
88	495	500	505
89	Leu Ser Ser Ala Ala Asn Asn Lys	Tyr Ala Lys Leu Ser	Gly Thr Ser
90	510	515	520
91	525	530	535
92	540	545	550
93	555	560	565
94	570	575	580
95	585	590	595
96	600	605	610
97	615	620	625
98	625	630	635
99	640		

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106 Ala Pro Lys Ala Leu Ile Glu Thr Ser Trp Gln Lys Ile Thr Ile Pro
 107 645 650 655
 108 Ala Asn Ser Ser Lys Gln Val Thr Ile Pro Ile Asp Ile Ser Gln Phe
 109 660 665 670
 110 Ser Lys Asp Leu Leu Ala Gln Met Lys Asn Gly Tyr Phe Leu Glu Gly
 111 675 680 685
 112 Phe Val Arg Ile Lys Gln Asp Pro Thr Lys Glu Glu Leu Met Ser Ile
 113 690 695 700
 114 Pro Tyr Ile Gly Phe Arg Gly Asp Phe Gly Asn Leu Ser Ala Leu Glu
 115 705 710 715 720
 116 Lys Pro Leu Tyr Asp Ser Lys Asp Gly Ser Ser Tyr Tyr His Glu Glu
 117 725 730 735
 118 Ile Ser Asp Ala Lys Asp Gln Leu Asp Gly Asp Gly Leu Gln Phe Tyr
 119 740 745 750
 120 Ala Leu Lys Asn Asp Phe Thr Ala Leu Thr Thr Glu Ser Asn Pro Trp
 121 755 760 765
 122 Thr Ile Ile Asn Val Val Lys Glu Gly Val Glu Asn Ile Glu Asp Ile
 123 770 775 780
 124 Glu Ser Ser Glu Ile Thr Glu Thr Ile Phe Ala Gly Thr Phe Ala Lys
 125 785 790 795 800
 126 Gln Asp Asp Asp Arg His Tyr Tyr Ile His Arg His Ala Asn Gly Lys
 127 805 810 815
 128 Pro Tyr Ala Ala Ile Ser Pro Asn Gly Asp Gly Asn Arg Asp Tyr Val
 129 820 825 830
 130 Gln Phe His Gly Thr Phe Leu Arg Asn Ala Lys Asn Leu Val Ala Glu
 131 835 840 845
 132 Val Leu Asp Lys Glu Gly Asn Val Val Trp Thr Ser Glu Val Thr Glu
 133 850 855 860
 134 Gln Val Val Lys Asn Tyr Asn Asn Asp Leu Ala Ser Thr Leu Gly Ser
 135 865 870 875 880
 136 Thr Arg Phe Glu Ile Ser Arg Trp Asp Gly Lys Asp Lys Asp Ala Lys
 137 885 890 895
 138 Val Val Ala Asn Gly Thr Tyr Thr Arg Val Arg Tyr Thr Pro Ile
 139 900 905 910
 140 Ser Ser Gly Ala Lys Glu Gln His Thr Asp Phe Asp Val Ile Val Asp
 141 915 920 925
 142 Asn Thr Thr Pro Glu Val Ala Thr Ser Ala Thr Phe Ser Thr Glu Asp
 143 930 935 940
 144 Arg Arg Leu Thr Leu Ala Ser Lys Pro Gln Thr Ser Gln Pro Val Tyr
 145 945 950 955 960
 146 Arg Glu Arg Ile Ala Tyr Thr Tyr Met Asp Glu Asp Leu Pro Thr Thr
 147 965 970 975
 148 Glu Tyr Ile Ser Pro Asn Glu Asp Gly Thr Phe Thr Leu Pro Glu Glu
 149 980 985 990
 150 Ala Glu Thr Met Glu Gly Ala Thr Val Pro Leu Lys Met Ser Asp Phe
 151 995 1000 1005
 152 Thr Tyr Val Val Glu Asp Met Ala Gly Asn Ile Thr Tyr Thr Pro Val
 153 1010 1015 1020
 154 Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp Gly Ser

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155 1025 1030 1035 1040
 156 Asp Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Gln Asp Gly
 157 1045 1050 1055
 158 Ser Asp Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Gly Gln Asp
 159 1060 1065 1070
 160 Gly Ser Gly Gln Thr Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Lys
 161 1075 1080 1085
 162 Asp Ser Ser Gly Gln Thr Pro Gly Lys Thr Pro Gln Lys Gly Gln Pro
 163 1090 1095 1100
 164 Ser Arg Thr Leu Glu Lys Arg Ser Ser Lys Arg Ala Leu Ala Thr Lys
 165 1105 1110 1115 1120
 166 Ala Ser Thr Arg Asp Gln Leu Pro Thr Thr Asn Asp Lys Asp Thr Asn
 167 1125 1130 1135
 168 Arg Leu His Leu Leu Lys Leu Val Met Thr Thr Phe Phe Leu Gly Leu
 169 1140 1145 1150
 170 Val Ala His Ile Phe Lys Thr Lys Arg Thr Glu Asp
 171 1155 1160
 173 <210> SEQ ID NO: 2
 174 <211> LENGTH: 1167
 175 <212> TYPE: PRT
 176 <213> ORGANISM: Streptococcus pyogenes
 178 <400> SEQUENCE: 2
 179 Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
 180 1 5 10 15
 181 Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
 182 20 25 30
 183 Thr Val Thr Glu Asp Thr Pro Val Thr Glu Gln Ala Val Glu Thr Pro
 184 35 40 45
 185 Gln Pro Thr Ala Val Ser Glu Glu Val Pro Ser Ser Lys Glu Thr Lys
 186 50 55 60
 187 Thr Pro Gln Thr Pro Asp Asp Ala Glu Glu Thr Ile Ala Asp Asp Ala
 188 65 70 75 80
 189 Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Ala Asp Thr Pro Ala
 190 85 90 95
 191 Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys
 192 100 105 110
 193 Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
 194 115 120 125
 195 Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
 196 130 135 140
 197 Lys Thr Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys
 198 145 150 155 160
 199 Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
 200 165 170 175
 201 Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu
 202 180 185 190
 203 His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
 204 195 200 205
 205 Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu

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206	210	215	220	
207	Leu	Leu	Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg	
208	225	230	235	240
209	Asn	Tyr Ala Gln Ala	Ile Arg Asp Ala Val Asn Leu Gly Ala Lys Val	
210	245	250	255	
211	Ile Asn Met Ser Phe Gly Asn Ala Ala	Leu Ala Tyr Ala Asn Leu Pro		
212	260	265	270	
213	Asp Glu Thr Lys Lys Ala Phe Asp Tyr Ala Lys Ser Lys Gly Val Ser			
214	275	280	285	
215	Ile Val Thr Ser Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg			
216	290	295	300	
217	Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala			
218	305	310	315	320
219	Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Lys Gln			
220	325	330	335	
221	Leu Thr Glu Thr Ala Met Val Lys Thr Asp Asp Gln Gln Asp Lys Glu			
222	340	345	350	
223	Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp			
224	355	360	365	
225	Tyr Ala Tyr Ala Asn Arg Gly Met Lys Glu Asp Asp Phe Lys Asp Val			
226	370	375	380	
227	Lys Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile Asp Phe Lys Asp			
228	385	390	395	400
229	Lys Val Ala Asn Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr			
230	405	410	415	
231	Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln			
232	420	425	430	
233	Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Lys Asp			
234	435	440	445	
235	Asn Pro Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro			
236	450	455	460	
237	Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr			
238	465	470	475	480
239	Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile			
240	485	490	495	
241	Leu Ser Ser Val Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser			
242	500	505	510	
243	Met Ser Ala Pro Leu Val Ala Gly Ile Met Gly Leu Leu Gln Lys Gln			
244	515	520	525	
245	Tyr Glu Thr Gln Tyr Pro Asp Met Thr Pro Ser Glu Arg Leu Asp Leu			
246	530	535	540	
247	Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp			
248	545	550	555	560
249	Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp			
250	565	570	575	
251	Ala Lys Lys Ala Ser Ala Ala Thr Met Tyr Val Thr Asp Lys Asp Asn			
252	580	585	590	
253	Thr Ser Ser Lys Val His Leu Asn Asn Val Ser Asp Lys Phe Glu Val			
254	595	600	605	

VERIFICATION SUMMARY

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DATE: 12/05/2001

TIME: 10:25:08

Input Set : A:\PCT-US99-28826 Sequence listing.txt.txt
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date